SEQUENCE LISTING

<110> Chan, Doug W
       Chen, Ping-Chi B
       Chen, David J

<120> DNA Dependent Protein Kinase Catalytic Subunit Phosphorylation Sites and Antibodies Thereto

<130> IB-1807 PCT

<140> US 10/511,561

<141> 2004-10-15

<150> US 60/375,094

<151> 2002-04-22

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<170> PatentIn version 3.1

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Met Ala Gly Ser Gly Ala Gly Val Arg Cys Ser Leu Leu Arg Leu Gln
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Glu Thr Leu Ser Ala Ala Asp Arg Cys Gly Ala Ala Leu Ala Gly His
            20   25   30

Gln Leu Ile Arg Gly Leu Gly Gln Glu Cys Val Leu Ser Ser Ser Pro
        35   40   45

Ala Val Leu Ala Leu Gln Thr Ser Leu Val Phe Ser Arg Asp Phe Gly
    50   55   60

Leu Leu Val Phe Val Arg Lys Ser Leu Asn Ser Ile Glu Phe Arg Glu
65   70   75   80

Cys Arg Glu Glu Ile Leu Lys Phe Leu Cys Ile Phe Leu Glu Lys Met
            85   90   95

Gly Gln Lys Ile Ala Pro Tyr Ser Val Glu Ile Lys Asn Thr Cys Thr
            100   105   110

Ser Val Tyr Thr Lys Asp Arg Ala Ala Lys Cys Lys Ile Pro Ala Leu
        115   120   125

Asp Leu Leu Ile Lys Leu Leu Gln Thr Phe Arg Ser Ser Arg Leu Met
    130   135   140

Asp Glu Phe Lys Ile Gly Glu Leu Phe Ser Lys Phe Tyr Gly Glu Leu
145   150   155   160

Ala Leu Lys Lys Lys Ile Pro Asp Thr Val Leu Glu Lys Val Tyr Glu
            165   170   175

Leu Leu Gly Leu Leu Gly Glu Val His Pro Ser Glu Met Ile Asn Asn
        180   185   190

Ala Glu Asn Leu Phe Arg Ala Phe Leu Gly Glu Leu Lys Thr Gln Met
        195   200   205

Thr Ser Ala Val Arg Glu Pro Lys Leu Pro Val Leu Ala Gly Cys Leu
        210   215   220

Lys Gly Leu Ser Ser Leu Leu Cys Asn Phe Thr Lys Ser Met Glu Glu
225   230   235   240

Asp Pro Gln Thr Ser Arg Glu Ile Phe Asn Phe Val Leu Lys Ala Ile
                245   250   255

Arg Pro Gln Ile Asp Leu Lys Arg Tyr Ala Val Pro Ser Ala Gly Leu
                260   265   270

Arg Leu Phe Ala Leu His Ala Ser Gln Phe Ser Thr Cys Leu Leu Asp
        275   280   285

Asn Tyr Val Ser Leu Phe Glu Val Leu Leu Lys Trp Cys Ala His Thr
        290   295   300

Asn Val Glu Leu Lys Lys Ala Ala Leu Ser Ala Leu Glu Ser Phe Leu
305   310   315   320

Lys Gln Val Ser Asn Met Val Ala Lys Asn Ala Glu Met His Lys Asn
                325   330   335

Lys Leu Gln Tyr Phe Met Glu Gln Phe Tyr Gly Ile Ile Arg Asn Val
                340   345   350

Asp Ser Asn Asn Lys Glu Leu Ser Ile Ala Ile Arg Gly Tyr Gly Leu
        355   360   365

Phe Ala Gly Pro Cys Lys Val Ile Asn Ala Lys Asp Val Asp Phe Met
        370   375   380

Tyr Val Glu Leu Ile Gln Arg Cys Lys Gln Met Phe Leu Thr Gln Thr
385   390   395   400

Asp Thr Gly Asp Tyr Arg Val Tyr Gln Met Pro Ser Phe Leu Gln Ser
                405   410   415

Val Ala Ser Val Leu Leu Tyr Leu Asp Thr Val Pro Glu Val Tyr Thr
        420   425   430

Pro Val Leu Glu His Leu Val Val Met Gln Ile Asp Ser Phe Pro Gln
        435   440   445

Tyr Ser Pro Lys Met Gln Leu Val Cys Cys Arg Ala Ile Val Lys Val
        450   455   460

Phe Leu Ala Leu Ala Ala Lys Gly Pro Val Leu Arg Asn Cys Ile Ser
465   470   475   480

Thr Val Val His Gln Gly Leu Ile Arg Ile Cys Ser Lys Pro Val Val
            485   490   495

Leu Pro Lys Gly Pro Glu Ser Glu Ser Glu Asp His Arg Ala Ser Gly
            500   505   510

Glu Val Arg Thr Gly Lys Trp Lys Val Pro Thr Tyr Lys Asp Tyr Val
            515   520   525

Asp Leu Phe Arg His Leu Leu Ser Ser Asp Gln Met Met Asp Ser Ile
        530   535   540

Leu Ala Asp Glu Ala Phe Phe Ser Val Asn Ser Ser Ser Glu Ser Leu
545   550   555   560

Asn His Leu Leu Tyr Asp Glu Phe Val Lys Ser Val Leu Lys Ile Val
            565   570   575

Glu Lys Leu Asp Leu Thr Leu Glu Ile Gln Thr Val Gly Glu Gln Glu
            580   585   590

Asn Gly Asp Glu Ala Pro Gly Val Trp Met Ile Pro Thr Ser Asp Pro
            595   600   605

Ala Ala Asn Leu His Pro Ala Lys Pro Lys Asp Phe Ser Ala Phe Ile
        610   615   620

Asn Leu Val Glu Phe Cys Arg Glu Ile Leu Pro Glu Lys Gln Ala Glu
625   630   635   640

Phe Phe Glu Pro Trp Val Tyr Ser Phe Ser Tyr Glu Leu Ile Leu Gln
            645   650   655

Ser Thr Arg Leu Pro Leu Ile Ser Gly Phe Tyr Lys Leu Leu Ser Ile
            660   665   670

Thr Val Arg Asn Ala Lys Lys Ile Lys Tyr Phe Glu Gly Val Ser Pro
        675   680   685

Lys Ser Leu Lys His Ser Pro Glu Asp Pro Glu Lys Tyr Ser Cys Phe
        690   695   700

Ala Leu Phe Val Lys Phe Gly Lys Glu Val Ala Val Lys Met Lys Gln
705   710   715   720

Tyr Lys Asp Glu Leu Leu Ala Ser Cys Leu Thr Phe Leu Leu Ser Leu
            725   730   735

Pro His Asn Ile Ile Glu Leu Asp Val Arg Ala Tyr Val Pro Ala Leu
            740   745   750

Gln Met Ala Phe Lys Leu Gly Leu Ser Tyr Thr Pro Leu Ala Glu Val
            755   760   765

Gly Leu Asn Ala Leu Glu Glu Trp Ser Ile Tyr Ile Asp Arg His Val
        770   775   780

Met Gln Pro Tyr Tyr Lys Asp Ile Leu Pro Cys Leu Asp Gly Tyr Leu
785   790   795   800

Lys Thr Ser Ala Leu Ser Asp Glu Thr Lys Asn Asn Trp Glu Val Ser
            805   810   815

Ala Leu Ser Arg Ala Ala Gln Lys Gly Phe Asn Lys Val Val Leu Lys
            820   825   830

His Leu Lys Lys Thr Lys Asn Leu Ser Ser Asn Glu Ala Ile Ser Leu
        835   840   845

Glu Glu Ile Arg Ile Arg Val Val Gln Met Leu Gly Ser Leu Gly Gly
        850   855   860

Gln Ile Asn Lys Asn Leu Leu Thr Val Thr Ser Ser Asp Glu Met Met
865   870   875   880

Lys Ser Tyr Val Ala Trp Asp Arg Glu Lys Arg Leu Ser Phe Ala Val
            885   890   895

Pro Phe Arg Glu Met Lys Pro Val Ile Phe Leu Asp Val Phe Leu Pro
        900   905   910

Arg Val Thr Glu Leu Ala Leu Thr Ala Ser Asp Arg Gln Thr Lys Val

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             915                    920                    925

Ala Ala Cys Glu Leu Leu His Ser Met Val Met Phe Met Leu Gly Lys
    930                 935                 940

Ala Thr Gln Met Pro Glu Gly Gly Gln Gly Ala Pro Pro Met Tyr Gln
945                 950                 955                 960

Leu Tyr Lys Arg Thr Phe Pro Val Leu Leu Arg Leu Ala Cys Asp Val
            965                 970                 975

Asp Gln Val Thr Arg Gln Leu Tyr Glu Pro Leu Val Met Gln Leu Ile
            980                 985                 990

His Trp Phe Thr Asn Asn Lys Lys  Phe Glu Ser Gln Asp  Thr Val Ser
        995                 1000                1005

Leu Leu  Glu Ala Ile Leu Asp  Gly Ile Val Asp Pro  Val Asp Ser
    1010                1015                1020

Thr Leu  Arg Asp Phe Cys Gly  Arg Cys Ile Arg Glu  Phe Leu Lys
    1025                1030                1035

Trp Ser  Ile Lys Gln Ile Thr  Pro Gln Gln Gln Glu  Lys Ser Pro
    1040                1045                1050

Val Asn  Thr Lys Ser Leu Phe  Lys Arg Leu Tyr Ser  Leu Ala Leu
    1055                1060                1065

His Pro  Asn Ala Phe Lys Arg  Leu Gly Ala Ser Leu  Ala Phe Asn
    1070                1075                1080

Asn Ile  Tyr Arg Glu Phe Arg  Glu Glu Glu Ser Leu  Val Glu Gln
    1085                1090                1095

Phe Val  Phe Glu Ala Leu Val  Ile Tyr Met Glu Ser  Leu Ala Leu
    1100                1105                1110

Ala His  Ala Asp Glu Lys Ser  Leu Gly Thr Ile Gln  Gln Cys Cys
    1115                1120                1125

Asp Ala  Ile Asp His Leu Cys  Arg Ile Ile Glu Lys  Lys His Val
    1130                1135                1140

Ser Leu  Asn Lys Ala Lys Lys  Arg Arg Leu Pro Arg  Gly Phe Pro
    1145                1150                1155
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Pro Ser Ala Ser Leu Cys Leu Leu Asp Leu Val Lys Trp Leu Leu
    1160   1165   1170

Ala His Cys Gly Arg Pro Gln Thr Glu Cys Arg His Lys Ser Ile
    1175   1180   1185

Glu Leu Phe Tyr Lys Phe Val Pro Leu Leu Pro Gly Asn Arg Ser
    1190   1195   1200

Pro Asn Leu Trp Leu Lys Asp Val Leu Lys Glu Glu Gly Val Ser
    1205   1210   1215

Phe Leu Ile Asn Thr Phe Glu Gly Gly Gly Cys Gly Gln Pro Ser
    1220   1225   1230

Gly Ile Leu Ala Gln Pro Thr Leu Leu Tyr Leu Arg Gly Pro Phe
    1235   1240   1245

Ser Leu Gln Ala Thr Leu Cys Trp Leu Asp Leu Leu Leu Ala Ala
    1250   1255   1260

Leu Glu Cys Tyr Asn Thr Phe Ile Gly Glu Arg Thr Val Gly Ala
    1265   1270   1275

Leu Gln Val Leu Gly Thr Glu Ala Gln Ser Ser Leu Leu Lys Ala
    1280   1285   1290

Val Ala Phe Phe Leu Glu Ser Ile Ala Met His Asp Ile Ile Ala
    1295   1300   1305

Ala Glu Lys Cys Phe Gly Thr Gly Ala Ala Gly Asn Arg Thr Ser
    1310   1315   1320

Pro Gln Glu Gly Glu Arg Tyr Asn Tyr Ser Lys Cys Thr Val Val
    1325   1330   1335

Val Arg Ile Met Glu Phe Thr Thr Thr Leu Leu Asn Thr Ser Pro
    1340   1345   1350

Glu Gly Trp Lys Leu Leu Lys Lys Asp Leu Cys Asn Thr His Leu
    1355   1360   1365

Met Arg Val Leu Val Gln Thr Leu Cys Glu Pro Ala Ser Ile Gly
    1370   1375   1380

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Phe Asn  Ile Gly Asp Val Gln  Val Met Ala His Leu  Pro Asp Val
    1385                1390            1395

Cys Val  Asn Leu Met Lys Ala  Leu Lys Met Ser Pro  Tyr Lys Asp
    1400                1405            1410

Ile Leu  Glu Thr His Leu Arg  Glu Lys Ile Thr Ala  Gln Ser Ile
    1415                1420            1425

Glu Glu  Leu Cys Ala Val Asn  Leu Tyr Gly Pro Asp  Ala Gln Val
    1430                1435            1440

Asp Arg  Ser Arg Leu Ala Ala  Val Val Ser Ala Cys  Lys Gln Leu
    1445                1450            1455

His Arg  Ala Gly Leu Leu His  Asn Ile Leu Pro Ser  Gln Ser Thr
    1460                1465            1470

Asp Leu  His His Ser Val Gly  Thr Glu Leu Leu Ser  Leu Val Tyr
    1475                1480            1485

Lys Gly  Ile Ala Pro Gly Asp  Glu Arg Gln Cys Leu  Pro Ser Leu
    1490                1495            1500

Asp Leu  Ser Cys Lys Gln Leu  Ala Ser Gly Leu Leu  Glu Leu Ala
    1505                1510            1515

Phe Ala  Phe Gly Gly Leu Cys  Glu Arg Leu Val Ser  Leu Leu Leu
    1520                1525            1530

Asn Pro  Ala Val Leu Ser Thr  Ala Ser Leu Gly Ser  Ser Gln Gly
    1535                1540            1545

Ser Val  Ile His Phe Ser His  Gly Glu Tyr Phe Tyr  Ser Leu Phe
    1550                1555            1560

Ser Glu  Thr Ile Asn Thr Glu  Leu Leu Lys Asn Leu  Asp Leu Ala
    1565                1570            1575

Val Leu  Glu Leu Met Gln Ser  Ser Val Asp Asn Thr  Lys Met Val
    1580                1585            1590

Ser Ala  Val Leu Asn Gly Met  Leu Asp Gln Ser Phe  Arg Glu Arg
    1595                1600            1605
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Ala Asn   Gln Lys His Gln Gly   Leu Lys Leu Ala Thr   Thr Ile Leu
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Gln His   Trp Lys Lys Cys Asp   Ser Trp Trp Ala Lys   Asp Ser Pro
    1625              1630                  1635

Leu Glu   Thr Lys Met Ala Val   Leu Ala Leu Leu Ala   Lys Ile Leu
    1640              1645                  1650

Gln Ile   Asp Ser Ser Val Ser   Phe Asn Thr Ser His   Gly Ser Phe
    1655              1660                  1665

Pro Glu   Val Phe Thr Thr Tyr   Ile Ser Leu Leu Ala   Asp Thr Lys
    1670              1675                  1680

Leu Asp   Leu His Leu Lys Gly   Gln Ala Val Thr Leu   Leu Pro Phe
    1685              1690                  1695

Phe Thr   Ser Leu Thr Gly Gly   Ser Leu Glu Glu Leu   Arg Arg Val
    1700              1705                  1710

Leu Glu   Gln Leu Ile Val Ala   His Phe Pro Met Gln   Ser Arg Glu
    1715              1720                  1725

Phe Pro   Pro Gly Thr Pro Arg   Phe Asn Asn Tyr Val   Asp Cys Met
    1730              1735                  1740

Lys Lys   Phe Leu Asp Ala Leu   Glu Leu Ser Gln Ser   Pro Met Leu
    1745              1750                  1755

Leu Glu   Leu Met Thr Glu Val   Leu Cys Arg Glu Gln   Gln His Val
    1760              1765                  1770

Met Glu   Glu Leu Phe Gln Ser   Ser Phe Arg Arg Ile   Ala Arg Arg
    1775              1780                  1785

Gly Ser   Cys Val Thr Gln Val   Gly Leu Leu Glu Ser   Val Tyr Glu
    1790              1795                  1800

Met Phe   Arg Lys Asp Asp Pro   Arg Leu Ser Phe Thr   Arg Gln Ser
    1805              1810                  1815

Phe Val   Asp Arg Ser Leu Leu   Thr Leu Leu Trp His   Cys Ser Leu
    1820              1825                  1830

Asp Ala   Leu Arg Glu Phe Phe   Ser Thr Ile Val Val   Asp Ala Ile
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        1835                    1840                    1845


Asp Val  Leu Lys Ser Arg Phe  Thr Lys Leu Asn Glu  Ser Thr Phe
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Asp Thr  Gln Ile Thr Lys Lys  Met Gly Tyr Tyr Lys  Ile Leu Asp
    1865                  1870                  1875


Val Met  Tyr Ser Arg Leu Pro  Lys Asp Asp Val His  Ala Lys Glu
    1880                  1885                  1890


Ser Lys  Ile Asn Gln Val Phe  His Gly Ser Cys Ile  Thr Glu Gly
    1895                  1900                  1905


Asn Glu  Leu Thr Lys Thr Leu  Ile Lys Leu Cys Tyr  Asp Ala Phe
    1910                  1915                  1920


Thr Glu  Asn Met Ala Gly Glu  Asn Gln Leu Leu Glu  Arg Arg Arg
    1925                  1930                  1935


Leu Tyr  His Cys Ala Ala Tyr  Asn Cys Ala Ile Ser  Val Ile Cys
    1940                  1945                  1950


Cys Val  Phe Asn Glu Leu Lys  Phe Tyr Gln Gly Phe  Leu Phe Ser
    1955                  1960                  1965


Glu Lys  Pro Glu Lys Asn Leu  Leu Ile Phe Glu Asn  Leu Ile Asp
    1970                  1975                  1980


Leu Lys  Arg Arg Tyr Asn Phe  Pro Val Glu Val Glu  Val Pro Met
    1985                  1990                  1995


Glu Arg  Lys Lys Lys Tyr Ile  Glu Ile Arg Lys Glu  Ala Arg Glu
    2000                  2005                  2010


Ala Ala  Asn Gly Asp Ser Asp  Gly Pro Ser Tyr Met  Ser Ser Leu
    2015                  2020                  2025


Ser Tyr  Leu Ala Asp Ser Thr  Leu Ser Glu Glu Met  Ser Gln Phe
    2030                  2035                  2040


Asp Phe  Ser Thr Gly Val Gln  Ser Tyr Ser Tyr Ser  Ser Gln Asp
    2045                  2050                  2055


Pro Arg  Pro Ala Thr Gly Arg  Phe Arg Arg Arg Glu  Gln Arg Asp
    2060                  2065                  2070
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Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu Leu
    2075   2080   2085

Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
    2090   2095   2100

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val
    2105   2110   2115

Pro Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu
    2120   2125   2130

Gly Asn Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys
    2135   2140   2145

Leu Val Ile Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His
    2150   2155   2160

Trp Leu Ser Pro Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly
    2165   2170   2175

Gly Glu Gly Ile His Tyr Met Val Val Glu Ile Val Ala Thr Ile
    2180   2185   2190

Leu Ser Trp Thr Gly Leu Ala Thr Pro Thr Gly Val Pro Lys Asp
    2195   2200   2205

Glu Val Leu Ala Asn Arg Leu Leu Asn Phe Leu Met Lys His Val
    2210   2215   2220

Phe His Pro Lys Arg Ala Val Phe Arg His Asn Leu Glu Ile Ile
    2225   2230   2235

Lys Thr Leu Val Glu Cys Trp Lys Asp Cys Leu Ser Ile Pro Tyr
    2240   2245   2250

Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys Asp Pro Asn Ser Lys
    2255   2260   2265

Asp Asn Ser Val Gly Ile Gln Leu Leu Gly Ile Val Met Ala Asn
    2270   2275   2280

Asp Leu Pro Pro Tyr Asp Pro Gln Cys Gly Ile Gln Ser Ser Glu
    2285   2290   2295

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Tyr Phe  Gln Ala Leu Val Asn  Asn Met Ser Phe Val  Arg Tyr Lys
    2300             2305             2310

Glu Val  Tyr Ala Ala Ala Ala  Glu Val Leu Gly Leu  Ile Leu Arg
    2315             2320             2325

Tyr Val  Met Glu Arg Lys Asn  Ile Leu Glu Glu Ser  Leu Cys Glu
    2330             2335             2340

Leu Val  Ala Lys Gln Leu Lys  Gln His Gln Asn Thr  Met Glu Asp
    2345             2350             2355

Lys Phe  Ile Val Cys Leu Asn  Lys Val Thr Lys Ser  Phe Pro Pro
    2360             2365             2370

Leu Ala  Asp Arg Phe Met Asn  Ala Val Phe Phe Leu  Leu Pro Lys
    2375             2380             2385

Phe His  Gly Val Leu Lys Thr  Leu Cys Leu Glu Val  Val Leu Cys
    2390             2395             2400

Arg Val  Glu Gly Met Thr Glu  Leu Tyr Phe Gln Leu  Lys Ser Lys
    2405             2410             2415

Asp Phe  Val Gln Val Met Arg  His Arg Asp Asp Glu  Arg Gln Lys
    2420             2425             2430

Val Cys  Leu Asp Ile Ile Tyr  Lys Met Met Pro Lys  Leu Lys Pro
    2435             2440             2445

Val Glu  Leu Arg Glu Leu Leu  Asn Pro Val Val Glu  Phe Val Ser
    2450             2455             2460

His Pro  Ser Thr Thr Cys Arg  Glu Gln Met Tyr Asn  Ile Leu Met
    2465             2470             2475

Trp Ile  His Asp Asn Tyr Arg  Asp Pro Glu Ser Glu  Thr Asp Asn
    2480             2485             2490

Asp Ser  Gln Glu Ile Phe Lys  Leu Ala Lys Asp Val  Leu Ile Gln
    2495             2500             2505

Gly Leu  Ile Asp Glu Asn Pro  Gly Leu Gln Leu Ile  Ile Arg Asn
    2510             2515             2520
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Phe Trp   Ser His Glu Thr Arg   Leu Pro Ser Asn Thr   Leu Asp Arg
    2525   2530   2535

Leu Leu   Ala Leu Asn Ser Leu   Tyr Ser Pro Lys Ile   Glu Val His
    2540   2545   2550

Phe Leu   Ser Leu Ala Thr Asn   Phe Leu Leu Glu Met   Thr Ser Met
    2555   2560   2565

Ser Pro   Asp Tyr Pro Asn Pro   Met Phe Glu His Pro   Leu Ser Glu
    2570   2575   2580

Cys Glu   Phe Gln Glu Tyr Thr   Ile Asp Ser Asp Trp   Arg Phe Arg
    2585   2590   2595

Ser Thr   Val Leu Thr Pro Met   Phe Val Glu Thr Gln   Ala Ser Gln
    2600   2605   2610

Gly Thr   Leu Gln Thr Arg Thr   Gln Glu Gly Ser Leu   Ser Ala Arg
    2615   2620   2625

Trp Pro   Val Ala Gly Gln Ile   Arg Ala Thr Gln Gln   Gln His Asp
    2630   2635   2640

Phe Thr   Leu Thr Gln Thr Ala   Asp Gly Arg Ser Ser   Phe Asp Trp
    2645   2650   2655

Leu Thr   Gly Ser Ser Thr Asp   Pro Leu Val Asp His   Thr Ser Pro
    2660   2665   2670

Ser Ser   Asp Ser Leu Leu Phe   Ala His Lys Arg Ser   Glu Arg Leu
    2675   2680   2685

Gln Arg   Ala Pro Leu Lys Ser   Val Gly Pro Asp Phe   Gly Lys Lys
    2690   2695   2700

Arg Leu   Gly Leu Pro Gly Asp   Glu Val Asp Asn Lys   Val Lys Gly
    2705   2710   2715

Ala Ala   Gly Arg Thr Asp Leu   Leu Arg Leu Arg Arg   Arg Phe Met
    2720   2725   2730

Arg Asp   Gln Glu Lys Leu Ser   Leu Met Tyr Ala Arg   Lys Gly Val
    2735   2740   2745

Ala Glu   Gln Lys Arg Glu Lys   Glu Ile Lys Ser Glu   Leu Lys Met

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      2750                    2755                    2760


Lys Gln  Asp Ala Gln Val Val  Leu Tyr Arg Ser Tyr  Arg His Gly
     2765                    2770                    2775


Asp Leu  Pro Asp Ile Gln Ile  Lys His Ser Ser Leu  Ile Thr Pro
     2780                    2785                    2790


Leu Gln  Ala Val Ala Gln Arg  Asp Pro Ile Ile Ala  Lys Gln Leu
     2795                    2800                    2805


Phe Ser  Ser Leu Phe Ser Gly  Ile Leu Lys Glu Met  Asp Lys Phe
     2810                    2815                    2820


Lys Thr  Leu Ser Glu Lys Asn  Asn Ile Thr Gln Lys  Leu Leu Gln
     2825                    2830                    2835


Asp Phe  Asn Arg Phe Leu Asn  Thr Thr Phe Ser Phe  Phe Pro Pro
     2840                    2845                    2850


Phe Val  Ser Cys Ile Gln Asp  Ile Ser Cys Gln His  Ala Ala Leu
     2855                    2860                    2865


Leu Ser  Leu Asp Pro Ala Ala  Val Ser Ala Gly Cys  Leu Ala Ser
     2870                    2875                    2880


Leu Gln  Gln Pro Val Gly Ile  Arg Leu Leu Glu Glu  Ala Leu Leu
     2885                    2890                    2895


Arg Leu  Leu Pro Ala Glu Leu  Pro Ala Lys Arg Val  Arg Gly Lys
     2900                    2905                    2910


Ala Arg  Leu Pro Pro Asp Val  Leu Arg Trp Val Glu  Leu Ala Lys
     2915                    2920                    2925


Leu Tyr  Arg Ser Ile Gly Glu  Tyr Asp Val Leu Arg  Gly Ile Phe
     2930                    2935                    2940


Thr Ser  Glu Ile Gly Thr Lys  Gln Ile Thr Gln Ser  Ala Leu Leu
     2945                    2950                    2955


Ala Glu  Ala Arg Ser Asp Tyr  Ser Glu Ala Ala Lys  Gln Tyr Asp
     2960                    2965                    2970


Glu Ala  Leu Asn Lys Gln Asp  Trp Val Asp Gly Glu  Pro Thr Glu
     2975                    2980                    2985
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Ala Glu Lys Asp Phe Trp Glu Leu Ala Ser Leu Asp Cys Tyr Asn
    2990   2995   3000

His Leu Ala Glu Trp Lys Ser Leu Glu Tyr Cys Ser Thr Ala Ser
    3005   3010   3015

Ile Asp Ser Glu Asn Pro Pro Asp Leu Asn Lys Ile Trp Ser Glu
    3020   3025   3030

Pro Phe Tyr Gln Glu Thr Tyr Leu Pro Tyr Met Ile Arg Ser Lys
    3035   3040   3045

Leu Lys Leu Leu Leu Gln Gly Glu Ala Asp Gln Ser Leu Leu Thr
    3050   3055   3060

Phe Ile Asp Lys Ala Met His Gly Glu Leu Gln Lys Ala Ile Leu
    3065   3070   3075

Glu Leu His Tyr Ser Gln Glu Leu Ser Leu Leu Tyr Leu Leu Gln
    3080   3085   3090

Asp Asp Val Asp Arg Ala Lys Tyr Tyr Ile Gln Asn Gly Ile Gln
    3095   3100   3105

Ser Phe Met Gln Asn Tyr Ser Ser Ile Asp Val Leu Leu His Gln
    3110   3115   3120

Ser Arg Leu Thr Lys Leu Gln Ser Val Gln Ala Leu Thr Glu Ile
    3125   3130   3135

Gln Glu Phe Ile Ser Phe Ile Ser Lys Gln Gly Asn Leu Ser Ser
    3140   3145   3150

Gln Val Pro Leu Lys Arg Leu Leu Asn Thr Trp Thr Asn Arg Tyr
    3155   3160   3165

Pro Asp Ala Lys Met Asp Pro Met Asn Ile Trp Asp Asp Ile Ile
    3170   3175   3180

Thr Asn Arg Cys Phe Phe Leu Ser Lys Ile Glu Glu Lys Leu Thr
    3185   3190   3195

Pro Leu Pro Glu Asp Asn Ser Met Asn Val Asp Gln Asp Gly Asp
    3200   3205   3210

Pro Ser Asp Arg Met Glu Val Gln Glu Gln Glu Glu Asp Ile Ser
    3215   3220   3225

Ser Leu Ile Arg Ser Cys Lys Phe Ser Met Lys Met Lys Met Ile
    3230   3235   3240

Asp Ser Ala Arg Lys Gln Asn Asn Phe Ser Leu Ala Met Lys Leu
    3245   3250   3255

Leu Lys Glu Leu His Lys Glu Ser Lys Thr Arg Asp Asp Trp Leu
    3260   3265   3270

Val Ser Trp Val Gln Ser Tyr Cys Arg Leu Ser His Cys Arg Ser
    3275   3280   3285

Arg Ser Gln Gly Cys Ser Glu Gln Val Leu Thr Val Leu Lys Thr
    3290   3295   3300

Val Ser Leu Leu Asp Glu Asn Asn Val Ser Ser Tyr Leu Ser Lys
    3305   3310   3315

Asn Ile Leu Ala Phe Arg Asp Gln Asn Ile Leu Leu Gly Thr Thr
    3320   3325   3330

Tyr Arg Ile Ile Ala Asn Ala Leu Ser Ser Glu Pro Ala Cys Leu
    3335   3340   3345

Ala Glu Ile Glu Glu Asp Lys Ala Arg Arg Ile Leu Glu Leu Ser
    3350   3355   3360

Gly Ser Ser Ser Glu Asp Ser Glu Lys Val Ile Ala Gly Leu Tyr
    3365   3370   3375

Gln Arg Ala Phe Gln His Leu Ser Glu Ala Val Gln Ala Ala Glu
    3380   3385   3390

Glu Glu Ala Gln Pro Pro Ser Trp Ser Cys Gly Pro Ala Ala Gly
    3395   3400   3405

Val Ile Asp Ala Tyr Met Thr Leu Ala Asp Phe Cys Asp Gln Gln
    3410   3415   3420

Leu Arg Lys Glu Glu Glu Asn Ala Ser Val Thr Asp Ser Ala Glu
    3425   3430   3435

Leu Gln Ala Tyr Pro Ala Leu Val Val Glu Lys Met Leu Lys Ala
    3440   3445   3450

Leu Lys Leu Asn Ser Asn Glu Ala Arg Leu Lys Phe Pro Arg Leu
    3455   3460   3465

Leu Gln Ile Ile Glu Arg Tyr Pro Glu Glu Thr Leu Ser Leu Met
    3470   3475   3480

Thr Lys Glu Ile Ser Ser Val Pro Cys Trp Gln Phe Ile Ser Trp
    3485   3490   3495

Ile Ser His Met Val Ala Leu Leu Asp Lys Asp Gln Ala Val Ala
    3500   3505   3510

Val Gln His Ser Val Glu Glu Ile Thr Asp Asn Tyr Pro Gln Ala
    3515   3520   3525

Ile Val Tyr Pro Phe Ile Ile Ser Ser Glu Ser Tyr Ser Phe Lys
    3530   3535   3540

Asp Thr Ser Thr Gly His Lys Asn Lys Glu Phe Val Ala Arg Ile
    3545   3550   3555

Lys Ser Lys Leu Asp Gln Gly Gly Val Ile Gln Asp Phe Ile Asn
    3560   3565   3570

Ala Leu Asp Gln Leu Ser Asn Pro Glu Leu Leu Phe Lys Asp Trp
    3575   3580   3585

Ser Asn Asp Val Arg Ala Glu Leu Ala Lys Thr Pro Val Asn Lys
    3590   3595   3600

Lys Asn Ile Glu Lys Met Tyr Glu Arg Met Tyr Ala Ala Leu Gly
    3605   3610   3615

Asp Pro Lys Ala Pro Gly Leu Gly Ala Phe Arg Arg Lys Phe Ile
    3620   3625   3630

Gln Thr Phe Gly Lys Glu Phe Asp Lys His Phe Gly Lys Gly Gly
    3635   3640   3645

Ser Lys Leu Leu Arg Met Lys Leu Ser Asp Phe Asn Asp Ile Thr
    3650   3655   3660

Asn Met Leu Leu Leu Lys Met Asn Lys Asp Ser Lys Pro Pro Gly

```
            3665                      3670                        3675


Asn Leu  Lys Glu Cys Ser Pro  Trp Met Ser Asp Phe  Lys Val Glu
    3680                  3685                  3690


Phe Leu  Arg Asn Glu Leu Glu  Ile Pro Gly Gln Tyr  Asp Gly Arg
    3695                  3700                  3705


Gly Lys  Pro Leu Pro Glu Tyr  His Val Arg Ile Ala  Gly Phe Asp
    3710                  3715                  3720


Glu Arg  Val Thr Val Met Ala  Ser Leu Arg Arg Pro  Lys Arg Ile
    3725                  3730                  3735


Ile Ile  Arg Gly His Asp Glu  Arg Glu His Pro Phe  Leu Val Lys
    3740                  3745                  3750


Gly Gly  Glu Asp Leu Arg Gln  Asp Gln Arg Val Glu  Gln Leu Phe
    3755                  3760                  3765


Gln Val  Met Asn Gly Ile Leu  Ala Gln Asp Ser Ala  Cys Ser Gln
    3770                  3775                  3780


Arg Ala  Leu Gln Leu Arg Thr  Tyr Ser Val Val Pro  Met Thr Ser
    3785                  3790                  3795


Arg Leu  Gly Leu Ile Glu Trp  Leu Glu Asn Thr Val  Thr Leu Lys
    3800                  3805                  3810


Asp Leu  Leu Leu Asn Thr Met  Ser Gln Glu Glu Lys  Ala Ala Tyr
    3815                  3820                  3825


Leu Ser  Asp Pro Arg Ala Pro  Pro Cys Glu Tyr Lys  Asp Trp Leu
    3830                  3835                  3840


Thr Lys  Met Ser Gly Lys His  Asp Val Gly Ala Tyr  Met Leu Met
    3845                  3850                  3855


Tyr Lys  Gly Ala Asn Arg Thr  Glu Thr Val Thr Ser  Phe Arg Lys
    3860                  3865                  3870


Arg Glu  Ser Lys Val Pro Ala  Asp Leu Leu Lys Arg  Ala Phe Val
    3875                  3880                  3885


Arg Met  Ser Thr Ser Pro Glu  Ala Phe Leu Ala Leu  Arg Ser His
    3890                  3895                  3900
```

```
Phe Ala  Ser Ser His Ala Leu  Ile Cys Ile Ser His  Trp Ile Leu
    3905             3910               3915

Gly Ile  Gly Asp Arg His Leu  Asn Asn Phe Met Val  Ala Met Glu
    3920             3925               3930

Thr Gly  Gly Val Ile Gly Ile  Asp Phe Gly His Ala  Phe Gly Ser
    3935             3940               3945

Ala Thr  Gln Phe Leu Pro Val  Pro Glu Leu Met Pro  Phe Arg Leu
    3950             3955               3960

Thr Arg  Gln Phe Ile Asn Leu  Met Leu Pro Met Lys  Glu Thr Gly
    3965             3970               3975

Leu Met  Tyr Ser Ile Met Val  His Ala Leu Arg Ala  Phe Arg Ser
    3980             3985               3990

Asp Pro  Gly Leu Leu Thr Asn  Thr Met Asp Val Phe  Val Lys Glu
    3995             4000               4005

Pro Ser  Phe Asp Trp Lys Asn  Phe Glu Gln Lys Met  Leu Lys Lys
    4010             4015               4020

Gly Gly  Ser Trp Ile Gln Glu  Ile Asn Val Ala Glu  Lys Asn Trp
    4025             4030               4035

Tyr Pro  Arg Gln Lys Ile Cys  Tyr Ala Lys Arg Lys  Leu Ala Gly
    4040             4045               4050

Ala Asn  Pro Ala Val Ile Thr  Cys Asp Glu Leu Leu  Leu Gly His
    4055             4060               4065

Glu Lys  Ala Pro Ala Phe Arg  Asp Tyr Val Ala Val  Ala Arg Gly
    4070             4075               4080

Ser Lys  Asp His Asn Ile Arg  Ala Gln Glu Pro Glu  Ser Gly Leu
    4085             4090               4095

Ser Glu  Glu Thr Gln Val Lys  Cys Leu Met Asp Gln  Ala Thr Asp
    4100             4105               4110

Pro Asn  Ile Leu Gly Arg Thr  Trp Glu Gly Trp Glu  Pro Trp Met
    4115             4120               4125
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<210> 4

<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (11)..(11)
<223> PHOSPHORYLATION at T2609

<400> 4

Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly
1   5   10   15

Thr Leu Gln Thr Arg
            20

<210> 5

<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(29)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (13)..(13)
<223> PHOSPHORYLATION at S2056

<400> 5

Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser Ser Gln Asp Pro
1   5   10   15

Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln Arg
            20   25

<210> 6

<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE

<222>   (1)..(303)
<223>   HUMAN GENETIC ORIGIN

<220>
<221>   MOD_RES
<222>   (177)..(177)
<223>   PHOSPHORYLATION at S2056

<400>   6

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1   5   10   15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
            20   25   30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
            35   40   45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
    50   55   60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65   70   75   80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
            85   90   95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
            100   105   110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
        115   120   125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
    130   135   140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145   150   155   160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
            165   170   175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
            180   185   190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
        195   200   205

```
Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
    210             215             220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225             230             235             240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
                245             250             255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
            260             265             270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
        275             280             285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile
    290             295             300
```

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<210>  7

<211>  388
<212>  PRT
<213>  Artificial Sequence

<220>
<221>  PEPTIDE
<222>  (1)..(388)
<223>  HUMAN GENETIC ORIGIN

<220>
<221>  MOD_RES
<222>  (177)..(177)
<223>  PHOSPHORYLATION at S2056

<400>  7
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```
Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1               5               10              15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
            20              25              30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
        35              40              45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
    50              55              60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65              70              75              80
```

```
Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
             85                  90                  95


Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
            100                 105             110


Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
            115                 120             125


Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
    130                 135                 140


Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145                 150                 155                 160


Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
                165                 170             175


Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
            180                 185                 190


Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
            195                 200             205


Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
    210                 215                 220


Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225                 230                 235                 240


Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
            245                 250                 255


Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
            260                 265                 270


Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
            275                 280                 285


Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile His
    290                 295                 300


Tyr Met Val Val Glu Ile Val Ala Thr Ile Leu Ser Trp Thr Gly Leu
305                 310                 315                 320
```

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu
                325   330   335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe
            340   345   350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp
        355   360   365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys
    370   375   380

Asp Pro Asn Ser
385

<210> 8

<211> 821
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(821)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (177)..(177)
<223> PHOSPHORYLATION at S2056

<220>
<221> MOD_RES
<222> (730)..(730)
<223> PHOSPHORYLATION at T2609

<400> 8

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1   5   10   15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
            20   25   30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
        35   40   45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
    50   55   60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
              85   90   95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
              100   105   110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Lys Tyr Ile Glu Ile
              115   120   125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
    130   135   140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145   150   155   160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
              165   170   175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln
              180   185   190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
              195   200   205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
    210   215   220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225   230   235   240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
              245   250   255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
              260   265   270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
              275   280   285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile His
    290   295   300

Tyr Met Val Val Glu Ile Val Ala Thr Ile Leu Ser Trp Thr Gly Leu
305   310   315   320

```
Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu
                325             330                 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe
            340             345                 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp
            355             360                 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys
    370             375                 380

Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu Leu Gly Ile
385             390                 395                     400

Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys Gly Ile Gln
                405                 410                 415

Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser Phe Val Arg
            420             425                 430

Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val Leu Gly Leu Ile Leu
        435             440                 445

Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser Leu Cys Glu
    450             455                 460

Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met Glu Asp Lys
465                 470                 475                 480

Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro Pro Leu Ala
            485             490                 495

Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys Phe His Gly
            500             505                 510

Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg Val Glu Gly
        515             520                 525

Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe Val Gln Val
    530             535                 540

Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu Asp Ile Ile

545                 550                 555                 560
```

Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg Glu Leu Leu
                565   570   575

Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr Cys Arg Glu
            580   585   590

Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr Arg Asp Pro
            595   600   605

Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys
    610   615   620

Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu
625   630   635   640

Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro Ser Asn Thr
                645   650   655

Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu
            660   665   670

Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu Met Thr Ser
            675   680   685

Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro Leu Ser Glu
    690   695   700

Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser
705   710   715   720

Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr
            725   730   735

Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val
            740   745   750

Ala Gly Gln Ile Arg Ala Thr Gln Gln His Asp Phe Thr Leu Thr
            755   760   765

Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser
    770   775   780

Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu
785   790   795   800

```
Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser
            805                 810                 815


Val Gly Pro Asp Phe
            820



<210>  9

<211>  440
<212>  PRT
<213>  Artificial Sequence

·<220>
<221>  PEPTIDE
<222>  (1)..(440)
<223>  HUMAN GENETIC ORIGIN

<220>
<221>  MOD_RES
<222>  (349)..(349)
<223>  PHOSPHORYLATION at T2609

<400>  9

Ser Gly Lys Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu
1               5                   10                  15


Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys
            20                  25                  30


Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser
            35                  40                  45


Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Glu Val Leu Gly
    50                  55                  60


Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser
65                  70                  75                  80


Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met
            85                  90                  95


Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro
            100                 105                 110


Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys
            115                 120                 125


Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg
    130                 135                 140
```

```
Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe
145                 150                 155                 160

Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu
                165                 170                 175

Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg
                180                 185                 190

Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr
                195                 200                 205

Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr
    210                 215                 220

Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys
225                 230                 235                 240

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
                245                 250                 255

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
                260                 265                 270

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
    275                 280                 285

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
    290                 295                 300

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
305                 310                 315                 320

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
                325                 330                 335

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
                340                 345                 350

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
    355                 360                 365

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
    370                 375                 380
```

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
385   390   395   400

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
                405   410   415

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
            420   425   430

Leu Lys Ser Val Gly Pro Asp Phe
            435   440

<210> 10
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(200)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (109)..(109)
<223> PHOSPHORYLATION at T2609

<400> 10

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
1   5   10   15

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
            20   25   30

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
            35   40   45

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
    50   55   60

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
65   70   75   80

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
            85   90   95

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
            100   105   110

```
Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
        115                 120             125

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
    130                 135             140

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
145                 150             155                 160

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
                165             170             175

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
            180             185             190

Leu Lys Ser Val Gly Pro Asp Phe
        195             200


<210>  11

<211>  428
<212>  PRT
<213>  Artificial Sequence

<220>
<221>  PEPTIDE
<222>  (1)..(428)
<223>  HUMAN GENETIC ORIGIN

<220>
<221>  MOD_RES
<222>  (335)..(335)
<223>  PHOSPHORYLATION at T2609

<400>  11

Gln Leu Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro
1               5               10              15

Gln Cys Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn
            20              25              30

Met Ser Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val
        35              40              45

Leu Gly Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu
    50              55              60

Glu Ser Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn
65              70              75              80
```

Thr Met Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser
                85   90   95

Phe Pro Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu
                100   105   110

Pro Lys Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu
                115   120   125

Cys Arg Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys
        130   135   140

Asp Phe Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val
145   150   155   160

Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu
                165   170   175

Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser
                180   185   190

Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp
                195   200   205

Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile
        210   215   220

Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn
225   230   235   240

Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg
                245   250   255

Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr
                260   265   270

Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu
                275   280   285

Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu
        290   295   300

His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp
305   310   315   320

Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln
            325   330   335

Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser
            340   345   350

Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His
            355   360   365

Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp
    370   375   380

Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser
385   390   395   400

Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg
            405   410   415

Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly Lys
            420   425

<210> 12

<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(273)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (180)..(180)
<223> PHOSPHORYLATION at T2609

<400> 12

Glu Arg Gln Lys Val Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys
1   5   10   15

Leu Lys Pro Val Glu Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe
            20   25   30

Val Ser His Pro Ser Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu
            35   40   45

Met Trp Ile His Asp Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn
    50   55   60

```
Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly
65                  70              75                      80


Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp
                85              90                      95


Ser His Glu Thr Arg Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala
            100             105                 110


Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu
            115             120                 125


Ala Thr Asn Phe Leu Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro
    130             135                 140


Asn Pro Met Phe Glu His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr
145             150                 155                     160


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Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln
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Glu Gly Ser Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala
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Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg
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Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp
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His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser
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Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln
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Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser
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tggctgacaa aaatgtcagg aaaacatgat gttggagctt acatgctaat gtataagggc    11640

gctaatcgta ctgaaacagt cacgtctttt agaaaacgag aaagtaaagt gcctgctgat    11700

ctcttaaagc gggccttcgt gaggatgagt acaagccctg aggctttcct ggcgctccgc    11760

tcccacttcg ccagctctca cgctctgata tgcatcagcc actggatcct cgggattgga    11820

gacagacatc tgaacaactt tatggtggcc atggagactg gcggcgtgat cgggatcgac    11880

tttgggcatg cgtttggatc cgctacacag tttctgccag tccctgagtt gatgcctttt    11940

cggctaactc gccagtttat caatctgatg ttaccaatga agaaacgggg ccttatgtac    12000

agcatcatgg tacacgcact ccgggccttc cgctcagacc ctggcctgct caccaacacc    12060

atggatgtgt ttgtcaagga gccctccttt gattggaaaa attttgaaca gaaaatgctg    12120

aaaaaaggag ggtcatggat tcaagaaata aatgttgctg aaaaaaattg gtacccccga    12180

cagaaaatat gttacgctaa gagaaagtta gcaggtgcca atccagcagt cattacttgt    12240

gatgagctac tcctgggtca tgagaaggcc cctgccttca gagactatgt ggctgtggca    12300

cgaggaagca agatcacaa cattcgtgcc caagaaccag agagtgggct ttcagaagag    12360

actcaagtga agtgcctgat ggaccaggca acagacccca acatccttgg cagaacctgg    12420

gaaggatggg agccctggat gtgaggtctg tgggagtctg cagatagaaa gcattacatt    12480

gtttaaagaa tctactatac tttggttggc agcattccat gagctgattt tcctgaaaca    12540

ctaaagagaa atgtcttttg tgctacagtt tcgtagcatg agtttaaatc aagattatga    12600

tgagtaaatg tgtatgggtt aaatcaaaga taaggttata gtaacatcaa agattaggtg    12660

aggtttatag aaagatagat atccaggctt accaaagtat taagtcaaga atataatatg    12720

tgatcagctt tcaaagcatt tacaagtgct gcaagttagt gaaacagctg tctccgtaaa    12780

tggaggaaat gtggggaagc cttggaatgc ccttctggtt ctggcacatt ggaaagcaca    12840

ctcagaaggc ttcatcacca agattttggg agagtaaagc taagtatagt tgatgtaaca    12900

ttgtagaagc agcataggaa caataagaac aataggtaaa gctataatta tggcttatat    12960

ttagaaatga ctgcatttga tattttagga tattttttcta ggttttttcc tttcattttta   13020
ttctcttcta gttttgacat tttatgatag atttgctctc tagaaggaaa cgtctttatt    13080
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taggagggca aaaattttgg tcatagcatt cacttttgct attccaatct acaactggaa    13140

gatacataaa agtgctttgc attgaatttg ggataacttc aaaaatccca tggttgttgt    13200

tagggatagt actaagcatt tcagttccag gagaataaaa gaaattccta tttgaaatga    13260

attcctcatt tggaggaaaa aaagcatgca ttctagcaca acaagatgaa attatggaat    13320

acaaaagtgg ctccttccca tgtgcagtcc ctgtccccc ccgccagtcc tccacaccca    13380

aactgtttct gattggcttt tagctttttg ttgttttttt ttttccttct aacacttgta    13440

tttggaggct cttctgtgat tttgagaagt atactcttga gtgtttaata aagttttttt    13500

ccaaaagta                                                          13509


<210>    16

<211>    63
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    cDNA sequence encoding the 2599-2619 peptide

<220>
<221>    CDS
<222>    (1)..(63)
<223>    HUMAN GENETIC ORIGIN

<220>
<221>    misc_feature
<222>    (31)..(33)
<223>    encodes T2609 residue

<400>    16

agtactgttc tcactccgat gtttgtggag acccaggcct cccagggcac tctccagacc        60

cgt                                                                      63


<210>    17

<211>    87
<212>    DNA
<213>    Artificial sequence

<220>
<223>    cDNA sequence encoding the 2044-2072 peptide

<220>
<221>    CDS
<222>    (1)..(87)
<223>    HUMAN GENETIC ORIGIN

<220>
<221>    misc_feature
<222>    (37)..(37)
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<223> encodes S2056 resdiue

<400> 17

gatttctcaa ccggagttca gagctattca tacagctccc aagaccctag acctgccact   60

ggtcgttttc ggagacggga gcagcgg   87

<210> 18

<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA sequence encoding the 1879-2182 peptide

<220>
<221> CDS
<222> (1)..(909)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (529)..(529)
<223> encodes S2056 residue

<400> 18

atgtattctc gccttcccaa agatgatgtt catgctaagg aatcaaaaat taatcaagtt   60

ttccatggct cgtgtattac agaaggaaat gaacttacaa agacattgat taaattgtgc   120

tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt   180

taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtta   240

aaattttacc aaggttttct gtttagtgaa aaaccagaaa gaacttgct tattttttgaa   300

aatctgatcg acctgaagcg ccgctataat tttcctgtag aagttgaggt tcctatggaa   360

agaaagaaaa agtacattga aattaggaaa gaagccagag aagcagcaaa tggggattca   420

gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa   480

atgagtcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct   540

agacctgcca ctggtcgttt tcggagacgg gagcagcggg accccacggt gcatgatgat   600

gtgctggagc tggagatgga cgagctcaat cggcatgagt gcatggcgcc cctgacggcc   660

ctggtcaagc acatgcacag aagcctgggc ccgcctcaag agaagagga ttcagtgcca   720

agagatcttc cttcttggat gaaattcctc catggcaaac tgggaaatcc aatagtacca   780

ttaaatatcc gtctcttctt agccaagctt gttattaata cagaagaggt ctttcgccct   840

tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga   900

gaaggaatt   909

<210> 19

<211> 1164
<212> DNA
<213> Artificial sequence

<220>
<223> Cloned DNA sequence encoding the 1879-2267 peptide

<220>
<221> CDS
<222> (1)..(1164)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (529)..(531)
<223> encodes S2056 residue

<400> 19

atgtattctc gccttcccaa agatgatgtt catgctaagg aatcaaaaat taatcaagtt   60

ttccatggct cgtgtattac agaaggaaat gaacttacaa agacattgat taaattgtgc   120

tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt   180

taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtta   240

aaattttacc aaggttttct gtttagtgaa aaaccagaaa agaacttgct tattttttgaa   300

aatctgatcg acctgaagcg ccgctataat tttcctgtag aagttgaggt tcctatggaa   360

agaaagaaaa agtacattga aattaggaaa gaagccagag aagcagcaaa tggggattca   420

gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa   480

atgagtcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct   540

agacctgcca ctggtcgttt tcggagacgg gagcagcggg accccacggt gcatgatgat   600

gtgctggagc tggagatgga cgagctcaat cggcatgagt gcatggcgcc cctgacggcc   660

ctggtcaagc acatgcacag aagcctgggc ccgcctcaag gagaagagga ttcagtgcca   720

agagatcttc cttcttggat gaaattcctc catggcaaac tgggaaatcc aatagtacca   780

ttaaatatcc gtctcttctt agccaagctt gttattaata cagaagaggt ctttcgccct   840

tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga   900

gaaggaattc actacatggt ggttgagata gtggccacta ttctttcatg gacaggcttg   960

gccactccaa cagggggtccc taaagatgaa gtgttagcaa atcgattgct taatttccta   1020

atgaaacatg tctttcatcc aaaaagagct gtgtttagac acaaccttga aattataaag   1080

acccttgtcg agtgctggaa ggattgttta tccatcccctt ataggttaat atttgaaaag   1140

ttttccggta aagatcctaa ttct   1164

<210>   20

<211>   2463
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   cDNA sequence encoding the 1879-2700 peptide

<220>
<221>   CDS
<222>   (1)..(2463)
<223>   HUMAN GENETIC ORIGIN

<220>
<221>   misc_feature
<222>   (529)..(531)
<223>   encodes S2056 residue

<220>
<221>   misc_feature
<222>   (2188)..(2190)
<223>   encodes T2609 residue

<400>   20

atgtattctc gccttcccaa agatgatgtt catgctaagg aatcaaaaat taatcaagtt   60

ttccatggct cgtgtattac agaaggaaat gaacttacaa agacattgat taaattgtgc   120

tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag agaagactt   180

taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagtta   240

aaattttacc aaggttttct gtttagtgaa aaaccagaaa agaacttgct tattttttgaa   300

aatctgatcg acctgaagcg ccgctataat tttcctgtag aagttgaggt tcctatggaa   360

agaaagaaaa agtacattga aattaggaaa gaagccagag aagcagcaaa tgggggattca   420

gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa   480

atgagtcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct   540

agacctgcca ctggtcgttt tcggagacgg gagcagcggg accccacggt gcatgatgat   600

gtgctggagc tggagatgga cgagctcaat cggcatgagt gcatggcgcc cctgacggcc   660

ctggtcaagc acatgcacag aagcctgggc ccgcctcaag agaagagga ttcagtgcca   720

agagatcttc cttcttggat gaaattcctc catggcaaac tgggaaatcc aatagtacca   780

ttaaatatcc gtctcttctt agccaagctt gttattaata cagaagaggt ctttcgccct   840

tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga   900

gaaggaattc actacatggt ggttgagata gtggccacta ttctttcatg gacaggcttg   960

```
gccactccaa cagggggtccc taaagatgaa gtgttagcaa atcgattgct taatttccta      1020

atgaaacatg tctttcatcc aaaaagagct gtgtttagac acaaccttga aattataaag      1080

acccttgtcg agtgctggaa ggattgttta tccatccctt ataggttaat atttgaaaag      1140

ttttccggta aagatcctaa ttctaaagac aactcagtag ggattcaatt gctaggcatc      1200

gtgatggcca atgacctgcc tccctatgac ccacagtgtg gcatccagag tagcgaatac      1260

ttccaggctt tggtgaataa tatgtccttt gtaagatata agaagtgta tgccgctgca       1320

gcagaagttc taggacttat acttcgatat gttatggaga gaaaaaacat actggaggag      1380

tctctgtgtg aactggttgc gaaacaattg aagcaacatc agaatactat ggaggacaag      1440

tttattgtgt gcttgaacaa agtgaccaag agcttccctc ctcttgcaga caggttcatg      1500

aatgctgtgt tctttctgct gccaaaattt catggagtgt tgaaaacact ctgtctggag      1560

gtggtacttt gtcgtgtgga gggaatgaca gagctgtact tccagttaaa gagcaaggac      1620

ttcgttcaag tcatgagaca tagagatgat gaaagacaaa aagtatgttt ggacataatt      1680

tataagatga tgccaaagtt aaaaccagta gaactccgag aacttctgaa ccccgttgtg      1740

gaattcgttt cccatccttc tacaacatgt agggaacaaa tgtataatat tctcatgtgg      1800

attcatgata attacagaga tccagaaagt gagacagata atgactccca ggaaatattt      1860

aagttggcaa aagatgtgct gattcaagga ttgatcgatg agaaccctgg acttcaatta      1920

attattcgaa atttctggag ccatgaaact aggttacctt caaataccctt ggaccggttg      1980

ctggcactaa attccttata ttctcctaag atagaagtgc acttttttaag tttagcaaca      2040

aattttctgc tcgaaatgac cagcatgagc ccagattatc caaaccccat gttcgagcat      2100

cctctgtcag aatgcgaatt tcaggaatat accattgatt ctgattggcg tttccgaagt      2160

actgttctca ctccgatgtt tgtggagacc caggcctccc agggcactct ccagacccgt      2220

acccaggaag ggtccctctc agctcgctgg ccagtggcag ggcagataag ggccacccag      2280

cagcagcatg acttcacact gacacagact gcagatggaa gaagctcatt tgattggctg      2340

accgggagca gcactgaccc gctggtcgac cacaccagtc cctcatctga ctccttgctg      2400

tttgcccaca agaggagtga aaggttacag agagcaccct tgaagtcagt ggggcctgat      2460

ttt                                                                    2463
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<210> 21

<211> 1320
<212> DNA
<213> Artificial sequence

<220>

<223> cDNA sequence encoding the 2261-2700 peptide

<220>
<221> CDS
<222> (1)..(1320)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (1045)..(1047)
<223> encodes T2609 residue

<400> 21

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tccggtaaag atcctaattc taaagacaac tcagtaggga ttcaattgct aggcatcgtg      60

atggccaatg acctgcctcc ctatgaccca cagtgtggca tccagagtag cgaatacttc     120

caggctttgg tgaataatat gtcctttgta agatataaag aagtgtatgc cgctgcagca     180

gaagttctag gacttatact tcgatatgtt atggagagaa aaaacatact ggaggagtct     240

ctgtgtgaac tggttgcgaa acaattgaag caacatcaga atactatgga ggacaagttt     300

attgtgtgct tgaacaaagt gaccaagagc ttccctcctc ttgcagacag gttcatgaat     360

gctgtgttct ttctgctgcc aaaatttcat ggagtgttga aaacactctg tctggaggtg     420

gtactttgtc gtgtggaggg aatgacagag ctgtacttcc agttaaagag caaggacttc     480

gttcaagtca tgagacatag agatgatgaa agacaaaaag tatgtttgga cataatttat     540

aagatgatgc caaagttaaa accagtagaa ctccgagaac ttctgaaccc cgttgtggaa     600

ttcgtttccc atccttctac aacatgtagg gaacaaatgt ataatattct catgtggatt     660

catgataatt acagagatcc agaaagtgag acagataatg actcccagga aatatttaag     720

ttggcaaaag atgtgctgat tcaaggattg atcgatgaga accctggact tcaattaatt     780

attcgaaatt tctggagcca tgaaactagg ttaccttcaa ataccttgga ccggttgctg     840

gcactaaatt ccttatattc tcctaagata gaagtgcact ttttaagttt agcaacaaat     900

tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct     960

ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact    1020

gttctcactc cgatgtttgt ggagacccag gcctcccagg cactctcca gacccgtacc    1080

caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc cacccagcag    1140

cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc    1200

gggagcagca ctgacccgct ggtcgaccac accagtccct catctgactc cttgctgttt    1260

gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt    1320
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<210> 22

<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA sequence encoding the 2500-2700 peptide

<220>
<221> CDS
<222> (1)..(600)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (325)..(327)
<223> encodes T2609 residue

<400> 22

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ttggcaaaag atgtgctgat tcaaggattg atcgatgaga accctggact tcaattaatt      60

attcgaaatt tctggagcca tgaaactagg ttaccttcaa ataccttgga ccggttgctg     120

gcactaaatt ccttatattc tcctaagata gaagtgcact ttttaagttt agcaacaaat     180

tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct     240

ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact     300

gttctcactc cgatgtttgt ggagacccag gcctcccagg cactctcca gacccgtacc     360

caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc cacccagcag     420

cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc     480

gggagcagca ctgacccgct ggtcgaccac accagtccct catctgactc cttgctgttt     540

gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt     600
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<210> 23

<211> 1284
<212> DNA
<213> Artificial sequence

<220>
<223> cDNA sequence encoding 2275-2702 peptide

<220>
<221> CDS
<222> (1)..(1284)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (1003)..(1005)
<223> encodes T2609 residue

<400> 23

caattgctag gcatcgtgat ggccaatgac ctgcctccct atgacccaca gtgtggcatc   60

cagagtagcg aatacttcca ggctttggtg aataatatgt cctttgtaag atataaagaa   120

gtgtatgccg ctgcagcaga agttctagga cttatacttc gatatgttat ggagagaaaa   180

aacatactgg aggagtctct gtgtgaactg gttgcgaaac aattgaagca acatcagaat   240

actatggagg acaagtttat tgtgtgcttg aacaaagtga ccaagagctt ccctcctctt   300

gcagacaggt tcatgaatgc tgtgttcttt ctgctgccaa aatttcatgg agtgttgaaa   360

acactctgtc tggaggtggt actttgtcgt gtggagggaa tgacagagct gtacttccag   420

ttaaagagca aggacttcgt tcaagtcatg agacatagag atgatgaaag acaaaaagta   480

tgtttggaca taatttataa gatgatgcca aagttaaaac cagtagaact ccgagaactt   540

ctgaaccccg ttgtggaatt cgtttcccat ccttctacaa catgtaggga caaatgtat   600

aatattctca tgtggattca tgataattac agagatccag aaagtgagac agataatgac   660

tcccaggaaa tatttaagtt ggcaaaagat gtgctgattc aaggattgat cgatgagaac   720

cctggacttc aattaattat tcgaaatttc tggagccatg aaactaggtt accttcaaat   780

accttggacc ggttgctggc actaaattcc ttatattctc ctaagataga agtgcacttt   840

ttaagtttag caacaaattt tctgctcgaa atgaccagca tgagcccaga ttatccaaac   900

cccatgttcg agcatcctct gtcagaatgc gaatttcagg aatataccat tgattctgat   960

tggcgtttcc gaagtactgt tctcactccg atgtttgtgg agacccaggc ctcccagggc   1020

actctccaga cccgtaccca ggaagggtcc ctctcagctc gctggccagt ggcagggcag   1080

ataagggcca cccagcagca gcatgacttc acactgacac agactgcaga tggaagaagc   1140

tcatttgatt ggctgaccgg gagcagcact gacccgctgg tcgaccacac cagtccctca   1200

tctgactcct tgctgtttgc ccacaagagg agtgaaaggt tacagagagc acccttgaag   1260

tcagtggggc ctgattttgg gaaa   1284

<210> 24

<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA sequence encoding 2429-2072 peptide

<220>
<221> CDS
<222> (1)..(819)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature

<222> (538)..(540)
<223> encodes T2609 residue

<400> 24

gaaagacaaa aagtatgttt ggacataatt tataagatga tgccaaagtt aaaaccagta   60

gaactccgag aacttctgaa ccccgttgtg gaattcgttt cccatccttc tacaacatgt   120

agggaacaaa tgtataatat tctcatgtgg attcatgata attacagaga tccagaaagt   180

gagacagata atgactccca ggaaatattt aagttggcaa agatgtgct gattcaagga   240

ttgatcgatg agaaccctgg acttcaatta attattcgaa atttctggag ccatgaaact   300

aggttacctt caaatacctt ggaccggttg ctggcactaa attccttata ttctcctaag   360

atagaagtgc acttttaag tttagcaaca aatttctgc tcgaaatgac cagcatgagc   420

ccagattatc caaaccccat gttcgagcat cctctgtcag aatgcgaatt tcaggaatat   480

accattgatt ctgattggcg tttccgaagt actgttctca ctccgatgtt tgtggagacc   540

caggcctccc agggcactct ccagacccgt acccaggaag ggtccctctc agctcgctgg   600

ccagtggcag ggcagataag ggccacccag cagcagcatg acttcacact gacacagact   660

gcagatggaa gaagctcatt tgattggctg accgggagca gcactgaccc gctggtcgac   720

cacaccagtc cctcatctga ctccttgctg tttgcccaca gaggagtga aaggttacag   780

agagcaccct tgaagtcagt ggggcctgat tttgggaaa   819

<210> 25

<211> 420
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA Sequence encoding 2561-2700 peptide

<220>
<221> CDS
<222> (1)..(420)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (145)..(147)
<223> Encodes T2609 residue

<400> 25

tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt cgagcatcct   60

ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcgttt ccgaagtact   120

gttctcactc cgatgtttgt ggagacccag gcctcccagg gcactctcca gacccgtacc   180

caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc cacccagcag   240

cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc   300

gggagcagca ctgacccgct ggtcgaccac accagtccct catctgactc cttgctgttt   360

gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt   420

<210>   26

<211>   306
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   cDNA sequence encoding 2600-2702 peptide

<220>
<221>   CDS
<222>   (1)..(306)
<223>   HUMAN GENETIC ORIGIN

<220>
<221>   misc_feature
<222>   (25)..(27)
<223>   Encodes T2609 residue

<400>   26

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caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc cacccagcag   120

cagcatgact tcacactgac acagactgca gatggaagaa gctcatttga ttggctgacc   180

gggagcagca ctgacccgct ggtcgaccac accagtccct catctgactc cttgctgttt   240

gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt   300

gggaaa   306

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<212>   DNA
<213>   Artificial sequence

<220>
<223>   Primer to create T2609A mutation

<400>   27

tccgatgttt gtggaggacc aggcctccca gggc   34

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<211>   34
<212>   DNA

<213>   Artificial Sequence

<220>
<223>   Reverse primer to create T2609A mutation

<400>   28

gccctgggag gcctggtcct ccacaaacat cgga   34